Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1. (Currently amended) A method for ~~introducing one or more mutations into a template double-stranded polynucleotide, wherein the template double-stranded polynucleotide has been cleaved into double-stranded random fragments of a desired size,~~ selecting or screening a library of recombinant proteins to identify a recombinant protein having a desired functional property, said method comprising:

a) randomly fragmenting a template double-stranded DNA into a plurality of double-stranded fragments of a desired size;

~~a~~b) adding to the resultant population of double-stranded fragments one or more single or double-stranded oligonucleotides, wherein said oligonucleotides comprise an area of identity and an area of heterology to the template polynucleotide;

~~b~~c) denaturing the resultant mixture of double-stranded random fragments and oligonucleotides into single-stranded fragments;

~~c~~d) incubating the resultant population of single-stranded fragments with a polymerase under conditions which result in the annealing of said single-stranded fragments at regions of identity, to form pairs of annealed fragments, said areas of identity being sufficient for one member of a pair to prime replication of the other thereby forming ~~between the single-stranded fragments and formation of a~~ mutagenized double-stranded ~~polynucleotides~~ DNA molecules; ~~and~~

~~d~~e) repeating steps (~~b~~c) and (~~c~~d) a desired number of times, wherein repeated step c) comprises denaturing the mutagenized double-stranded DNA molecules from step d) of the previous cycle to form a library of mutagnized double-stranded DNA molecules;

f) expressing a library of recombinant proteins from the library of mutagenized double-stranded DNA from step e); and

g) selecting or screening the library of recombinant proteins to identify a recombinant protein with a desired functional property.

2. (Original) The method of Claim 1 wherein the concentration of a specific double-stranded fragment in the mixture of double-stranded fragments is less than 1% by weight of the total DNA.

3. (Original) The method of Claim 1 wherein the number of different specific double-stranded fragments comprises at least about 100.

4. (Original) The method of Claim 1 wherein the size of the double-stranded fragments is from about 5 bp to 5 kb.

5. (Currently amended) The method of Claim 1 wherein the size of the mutagenized double-stranded DNA molecules in the library of ~~size of the~~ mutagenized ~~template~~ double-stranded ~~polynucleotide~~ DNA molecules ~~comprises~~ is from about 50 bp to 100 kb.

Claims 6-32 (Cancelled)

33. (New) The method of Claim 1, wherein the template double-stranded polynucleotide encodes a wild-type protein.

34. (New) The method of Claim 1, wherein the polymerase is Taq.

35. (New) The method of Claim 1, wherein the polymerase is Klenow polymerase.

36. (New) The method of Claim 1, wherein the template double-stranded DNA is from 50 bp to 50 kb.

37. (New) The method of Claim 1, wherein the size of the double-stranded fragments is from about 10 bp to 1000 bp.

38. (New) The method of Claim 1, wherein the size of the double-stranded fragments is from about 20 bp to 500 bp.